

1 GCGGCCGCGAATTCGGCACCCAGGGGCGCTCTCTCCCGGTGTGGGTACTGCTGTCTGTGGT 60  
 -----+-----+-----+-----+-----+-----+-----+  
 61 GTGGCTGTGGGACCCGTGAGCAAGCAGCGACGCCAGCGGCGGAGAACCGACGAAAGGTGT 120  
 -----+-----+-----+-----+-----+-----+-----+  
 121 CACCACAGTGATGGCAGTGGAGGACAGCACGCTGCAAGTAGTGGTACGGGTGCGGCCCCC 180  
 -----+-----+-----+-----+-----+-----+-----+  
 MetAlaValGluAspSerThrLeuGlnValValValArgValArgProPr  
 181 CACCCCTCGGGAGCTGGACAGTCAGCGGCGGCCAGTGGTTCAGGTGGTGGACGAGCGGGT 240  
 -----+-----+-----+-----+-----+-----+-----+  
 oThrProArgGluLeuAspSerGlnArgArgProValValGlnValValAspGluArgVa  
 241 GCTGGTGTTTAACCCTGAGGAGCCCGATGGAGGGTTCCTGGCCTGAAATGGGGTGGCAC 300  
 -----+-----+-----+-----+-----+-----+-----+  
 lLeuValPheAsnProGluGluProAspGlyGlyPheProGlyLeuLysTrpGlyGlyTh  
 301 CCATGATGGCCCCAAGAAGAAGGGCAAAGACCTGACGTTTGTCTTTGACCGGGTCTTTGG 360  
 -----+-----+-----+-----+-----+-----+-----+  
 rHisAspGlyProLysLysLysGlyLysAspLeuThrPheValPheAspArgValPheGl  
 361 CGAGGCGGCCACCCAACAGGACGTGTTCCAGCACACCACGCACAGCGTCCTGGACAGCTT 420  
 -----+-----+-----+-----+-----+-----+-----+  
 yGluAlaAlaThrGlnGlnAspValPheGlnHisThrThrHisSerValLeuAspSerPh  
 421 CCTCCAGGGCTACAACCTGCTCAGTGTTCCTACGGGGCCACCGGGGCTGGGAAGACACA 480  
 -----+-----+-----+-----+-----+-----+-----+  
 eLeuGlnGlyTyrAsnCysSerValPheAlaTyrGlyAlaThrGlyAlaGlyLysThrHi  
 481 CACCATGCTGGGAAGGGAGGGGGACCCCGGCATCATGTACCTGACCACCGTGGAAGTGT 520  
 -----+-----+-----+-----+-----+-----+-----+  
 sThrMetLeuGlyArgGluGlyAspProGlyIleMetTyrLeuThrThrValGluLeuTy  
 541 CAGGCGCCTGGAGGCCCGCCAGCAGGAGAAGCACTTCGAGGTGCTCATCAGCTACCAGGA 600  
 -----+-----+-----+-----+-----+-----+-----+  
 rArgArgLeuGluAlaArgGlnGlnGluLysHisPheGluValLeuIleSerTyrGlnGl

FIG. 1A

601 GGTGTATAATGAACAGATCCATGACCTCCTGGAGCCCAAGGGGCCCTTGCCATCCGCGA 660  
 -----+-----+-----+-----+-----+-----+-----+  
 uValTyrAsnGluGlnIleHisAspLeuLeuGluProLysGlyProLeuAlaIleArgGlu

661 GGACCCCGACAAGGGGGTGGTGGTGAAGGACTTTCTTTCCACCAGCCAGCCTCAGCCGA 720  
 -----+-----+-----+-----+-----+-----+-----+  
 uAspProAspLysGlyValValValGlnGlyLeuSerPheHisGlnProAlaSerAlaGlu

721 GCAGCTGCTGGAGATACTGACCAGGGGGAACCGTAACCGCACGCAGCACCCCACTGATGC 780  
 -----+-----+-----+-----+-----+-----+-----+  
 uGlnLeuLeuGluIleLeuThrArgGlyAsnArgAsnArgThrGlnHisProThrAspAla

781 CAACGCGACTTCCTCCCGCTCCCATGCCATCTTCCAGATCTTTGTGAAGCAGCAGGACCG 840  
 -----+-----+-----+-----+-----+-----+-----+  
 aAsnAlaThrSerSerArgSerHisAlaIlePheGlnIlePheValLysGlnGlnAspArg

841 GGTTCAGGACTGACCCAGGCTGTCCAGGTGGCCAAGATGAGCCTGATTGACCTGGCTGG 900  
 -----+-----+-----+-----+-----+-----+-----+  
 gValProGlyLeuThrGlnAlaValGlnValAlaLysMetSerLeuIleAspLeuAlaGlu

901 CTCAGAGCGGGCATCCAGCACCCATGCGAAGGGGGAGCGGCTGCGGGAGGGGGCCAACAT 960  
 -----+-----+-----+-----+-----+-----+-----+  
 ySerGluArgAlaSerSerThrHisAlaLysGlyGluArgLeuArgGluGlyAlaAsnIle

961 CAACCGCTCTCTGCTGGCGCTCATCAACGTCCTCAATGCCTTGGCCGATGCAAAGGGCCG 1020  
 -----+-----+-----+-----+-----+-----+-----+  
 eAsnArgSerLeuLeuAlaLeuIleAsnValLeuAsnAlaLeuAlaAspAlaLysGlyArg

1021 CAAGACCCATGTGCCCTACCGGGACAGCAAACCTGACCCGCCTGCTCAAAGACTCCCTCGG 1080  
 -----+-----+-----+-----+-----+-----+-----+  
 gLysThrHisValProTyrArgAspSerLysLeuThrArgLeuLeuLysAspSerLeuGlu

1081 GGGCAACTGCCGCACAGTGATGATCGCTGCCATCAGCCCCTCCAGCCTGACCTACGAGGA 1120  
 -----+-----+-----+-----+-----+-----+-----+  
 yGlyAsnCysArgThrValMetIleAlaAlaIleSerProSerSerLeuThrTyrGluAsp

1141 CACGTACAACACCCTCAAATATGCCGACCGGGCCAAGGAGATCAGGCTCTCGCTGAAGAG 1200  
 -----+-----+-----+-----+-----+-----+-----+  
 pThrTyrAsnThrLeuLysTyrAlaAspArgAlaLysGluIleArgLeuSerLeuLysSer

1201 CAATGTGACCAGCCTGGACTGTCACATCAGCCAGTATGCTACCATCTGCCAACAGCTCCA 1260  
 -----+-----+-----+-----+-----+-----+-----+  
 rAsnValThrSerLeuAspCysHisIleSerGlnTyrAlaThrIleCysGlnGlnLeuGlu

FIG. 1B

1261 GGCTGAGGTAGCCGCTCTGAGGAAGAAGCTCCAAGTGTATGAGGGGGGAGGCCAGCCCCC 1320  
 -----+-----+-----+-----+-----+-----+-----+ 1320  
 nAlaGluValAlaAlaLeuArgLysLysLeuGlnValTyrGluGlyGlyGlyGlnProPr

1321 ACCACAGGACCTCCCAGGATCTCCCAAGTCGGGACCACCACCAGAACACCTTCCCAGCTC 1380  
 -----+-----+-----+-----+-----+-----+-----+ 1380  
 oProGlnAspLeuProGlySerProLysSerGlyProProProGluHisLeuProSerSe

1381 CCCCTTGCCACCCACCCTCCCAGCCAGCCCTGCACCCCAGAGCTCCCTGCAGGGCCTAG 1440  
 -----+-----+-----+-----+-----+-----+-----+ 1440  
 rProLeuProProHisProProSerGlnProCysThrProGluLeuProAlaGlyProAr

1441 AGCCCTTCAAGAGGAGAGTCTGGGGATGGAGGCCCAGGTGGAGAGGGCCATGGAAGGGAA 1500  
 -----+-----+-----+-----+-----+-----+-----+ 1500  
 gAlaLeuGlnGluGluSerLeuGlyMetGluAlaGlnValGluArgAlaMetGluGlyAs

1501 CTCTTCAGACCAGGAGCAGTCCCCAGAGGATGAGGATGAAGGCCCAGCTGAGGAGGTTCC 1560  
 -----+-----+-----+-----+-----+-----+-----+ 1560  
 nSerSerAspGlnGluGlnSerProGluAspGluAspGluGlyProAlaGluGluValPr

1561 AACCCAGATGCCAGAGCAGAACCCACACATGCACTGCCAGAGTCCCCTCGCCTGACCCT 1620  
 -----+-----+-----+-----+-----+-----+-----+ 1620  
 oThrGlnMetProGluGlnAsnProThrHisAlaLeuProGluSerProArgLeuThrLe

1621 GCAGCCCAAGCCAGTCGTGGGCCACTTCTCAGCACGGGAACCTGGATGGGGACCGTTCTAA 1680  
 -----+-----+-----+-----+-----+-----+-----+ 1680  
 uGlnProLysProValValGlyHisPheSerAlaArgGluLeuAspGlyAspArgSerLy

1681 GCAGTTGGCCCTAAAGGTGCTGTGCGTTGCCAGCGGCAGTACTCCCTGCTCCAAGCAGC 1740  
 -----+-----+-----+-----+-----+-----+-----+ 1740  
 sGlnLeuAlaLeuLysValLeuCysValAlaGlnArgGlnTyrSerLeuLeuGlnAlaAl

1741 CAACCTCCTGACGCCCCGACATGATCACAGAGTTTGAGACCCTACAGCAGCTGGTGCAAGA 1800  
 -----+-----+-----+-----+-----+-----+-----+ 1800  
 aAsnLeuLeuThrProAspMetIleThrGluPheGluThrLeuGlnGlnLeuValGlnGl

1801 GGAAAAAATTGAGCCTGGGGCAGAGGCCTTGAGGACTTCAGGCCTGGCCAGGGGGGCACC 1860  
 -----+-----+-----+-----+-----+-----+-----+ 1860  
 uGluLysIleGluProGlyAlaGluAlaLeuArgThrSerGlyLeuAlaArgGlyAlaPr

1861 TCTGGCTCAGGAGCTGTGTTTCAGAGTCAATCCCTGTGCCGTCTCCTCTCTGCCAGAGCC 1920  
 -----+-----+-----+-----+-----+-----+-----+ 1920  
 oLeuAlaGlnGluLeuCysSerGluSerIleProValProSerProLeuCysProGluPr

FIG. 1C

1921 TCCAGGATACACTGGCCCTGTGACCCGGACTATGGCGAGGCGACTGAGTGGCCCCCTGCA 1980  
 -----+-----+-----+-----+-----+-----+-----+  
 oProGlyTyrThrGlyProValThrArgThrMetAlaArgArgLeuSerGlyProLeuHi  
  
 1981 CACCCCTGGGAATCCCGCCTGGACCCAACCTGCACCCCAGCCCAGGGGTCCCGATGGCCCCAT 2040  
 -----+-----+-----+-----+-----+-----+-----+  
 sThrLeuGlyIleProProGlyProAsnCysThrProAlaGlnGlySerArgTrpProMe  
  
 2041 GGAGAAGAAGAGGAGGAGACCAAGCGCCTTGGAGGCAGACAGTCCCATGGCCTCAAAGCG 2100  
 -----+-----+-----+-----+-----+-----+-----+  
 tGluLysLysArgArgArgProSerAlaLeuGluAlaAspSerProMetAlaSerLysAr  
  
 2101 GGGCACCAAGCGCCAGCGCCAGTCCTTCCTGCCCTGCCTAAGGAGAGGGTCTCTGCCTGA 2160  
 -----+-----+-----+-----+-----+-----+-----+  
 gGlyThrLysArgGlnArgGlnSerPheLeuProCysLeuArgArgGlySerLeuProAs  
  
 2161 CACCCAACCTTCACAGGGGGCCAGCACCCCCAAAGGAGAAAGGGCCTCCTCCCCCTGCCA 2220  
 -----+-----+-----+-----+-----+-----+-----+  
 pThrGlnProSerGlnGlyProSerThrProLysGlyGluArgAlaSerSerProCysHi  
  
 2221 TTCCCCTCGCGTTTGGCCAGCCACAGTCATCAAAAGCCGGGTGCCCCTGGGCCCCTCCGC 2280  
 -----+-----+-----+-----+-----+-----+-----+  
 sSerProArgValCysProAlaThrValIleLysSerArgValProLeuGlyProSerAl  
  
 2281 CATGCAGAACTGCTCCACCCCGCTGGCTCTGCCCACTCGAGACCTCAATGCCACCTTTGA 2340  
 -----+-----+-----+-----+-----+-----+-----+  
 aMetGlnAsnCysSerThrProLeuAlaLeuProThrArgAspLeuAsnAlaThrPheAs  
  
 2341 TCTCTCTGAGGAGCCTCCCTCAAAGCCCAGTTTCCATGAATGCATTGGCTGGGACAAAAT 2400  
 -----+-----+-----+-----+-----+-----+-----+  
 pLeuSerGluGluProProSerLysProSerPheHisGluCysIleGlyTrpAspLysIl  
  
 2401 ACCCCAGGAGCTGAGCAGGCTGGACCAGCCCTTCATCCCCAGGGCACCTGTGCCCTGTT 2460  
 -----+-----+-----+-----+-----+-----+-----+  
 eProGlnGluLeuSerArgLeuAspGlnProPheIleProArgAlaProValProLeuPh  
  
 2461 CACCATGAAGGGCCCCAAGCCAACATCTTCCCTCCCTGGGACCTCTGCCTGCAAGAAGAA 2520  
 -----+-----+-----+-----+-----+-----+-----+  
 eThrMetLysGlyProLysProThrSerSerLeuProGlyThrSerAlaCysLysLysLy  
  
 2521 GCGCGTTGCGAGTTCCTCAGTCTCCCATGGCCGCGCCGCATCGCCCGCCTCCCCAGCAG 2580  
 -----+-----+-----+-----+-----+-----+-----+  
 sArgValAlaSerSerSerValSerHisGlyArgSerArgIleAlaArgLeuProSerSe

FIG. 1D

2581 CACTTTGAAGAGGCCAGCTGGGCCCCTTGTACTCCCAGAGCTGCCCTTGAGTCCCCTGTG 2640  
 -----+-----+-----+-----+-----+-----+-----+  
 rThrLeuLysArgProAlaGlyProLeuValLeuProGluLeuProLeuSerProLeuCy  
 2641 CCCTAGCAACCGGAGGAATGGAAAGGACCTCATCAGGGTGGGGAGAGCGCTCTCAGCAGG 2700  
 -----+-----+-----+-----+-----+-----+-----+  
 sProSerAsnArgArgAsnGlyLysAspLeuIleArgValGlyArgAlaLeuSerAlaGl  
 2701 GAACGGCGTCACCAAGGTGTCCTGACCGCCAGAATGTCCTGACCACCAAGGTGTCCTAAC 2760  
 -----+-----+-----+-----+-----+-----+-----+  
 yAsnGlyValThrLysValSer  
 2761 CTACCGGCCCCTCTGCTGGATACCCCTCTTGACCTGTAGCCACCTGCACCAGGAGCTGG 2820  
 -----+-----+-----+-----+-----+-----+-----+  
 2821 ACCTGCCTTCCTTACCTGGGAGCAATTAGTGCCAACACACCTTTGCTGTATTAACATCCC 2880  
 -----+-----+-----+-----+-----+-----+-----+  
 2881 TCCCCAGACATCCATCCTGCTACTCACCCCTCTGTTAATCTCCTGTTACACTCAGCTTCTT 2940  
 -----+-----+-----+-----+-----+-----+-----+  
 2941 GGCATGTACATATTCATTTGTGAGTGTTAATGTGCTGCTGTTTTTTGTTTTTTGGTGGTT 3000  
 -----+-----+-----+-----+-----+-----+-----+  
 3001 TTTGTTTTTTGTTTTTTTGTGAGATGGAGTCTTACTCTGTCGCCCAGGCTGGAGTG 3060  
 -----+-----+-----+-----+-----+-----+-----+  
 3061 CAGTGGTACGATCTTGGCTCACTGCAACCTCCGCCTCCTGGGTTCAGTAATTCTCCTGC 3120  
 -----+-----+-----+-----+-----+-----+-----+  
 3121 CTCAGCTTTCCAAGTAGCTGGGATTACAGGCACCCATCACCACACCCAGCTAATTTTCGT 3180  
 -----+-----+-----+-----+-----+-----+-----+  
 3181 CTTTTTAATAGAGAGGGGGTTTTTCCATGTTGGCCAGGCTGGTCTTGAACCTCCTGACCTC 3240  
 -----+-----+-----+-----+-----+-----+-----+  
 3241 AGGTGATCCGCCTGCCTCAGCTTCCCAAAGTGCTGAGATTACAGGCATGAGCTACCACGC 3300  
 -----+-----+-----+-----+-----+-----+-----+  
 3301 CTGGCCCGTGTTGCTGTTTTAAAGGTGCTGCCATGTTCCCCCATCTTTTTTTTTTTTGGAG 3360  
 -----+-----+-----+-----+-----+-----+-----+

FIG. 1E

3361 ATGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGTGGCGATCTTGGCTCACTGCA 3420  
 -----+-----+-----+-----+-----+-----+-----+  
 3421 AGCTCCGCCTCCCAGGTTACACCATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTA 3480  
 -----+-----+-----+-----+-----+-----+-----+  
 3481 CAGGCGCCCACCACCACGCCCGGCTAATTTTTTGTATTTTGTAGTAGAGATGGGGTTTCAC 3540  
 -----+-----+-----+-----+-----+-----+-----+  
 3541 CGTGTTAGCCAGGCTGGTCTCGATCTGACCTCATGATCCACCCGCCTCGGCCTCCCAAAG 3600  
 -----+-----+-----+-----+-----+-----+-----+  
 3601 TGCTGGGATTACAGGCGTGAGCCACTGCGCCCGGCCTCCCCTCTCATTTATGATGCCCTC 3660  
 -----+-----+-----+-----+-----+-----+-----+  
 3661 TGTGCAGGCAGACGGCTCTTGGGCTCTTTTCCCCACCTGTCTCTAACACAGGCCCCACGG 3720  
 -----+-----+-----+-----+-----+-----+-----+  
 3721 TGATGGCCACAGGCAGTAGAGGAGGAATGAGGATGGGTGGGGAGCGGGGAGTCGCGGCT 3780  
 -----+-----+-----+-----+-----+-----+-----+  
 3781 TGGCTCTTCCTGGTTTCTGAGAGGGACATCTTCATCCCTACTCCCCTTGGTCCCCAACCA 3840  
 -----+-----+-----+-----+-----+-----+-----+  
 3841 CAGTCCTGGTGAAGATGTGGATGATAATGGTGCCTTGATTTCCAAATGAAGACAGCTTTA 3900  
 -----+-----+-----+-----+-----+-----+-----+  
 3901 TTGCTTAACTCTATTGTACATAGGATACACGTTCAGTGTAATAAAGTGTAAGGGGAA 3960  
 -----+-----+-----+-----+-----+-----+-----+  
 3961 TTCAGGCTTAATGCTGCACCTAGATATAAATGCTAATGATACTTGGGTTTATAGCCTTCT 4020  
 -----+-----+-----+-----+-----+-----+-----+  
 4021 GATCCTTTATTTCTGCATATATATAGATATATACATATATTTTGGTATAACAATAAA 4080  
 -----+-----+-----+-----+-----+-----+-----+  
 4081 CCGTCTCCATCCTTGGGAAAAAAAAAAAA 4108  
 -----+-----+-----+-----+-----+-----+-----+

FIG. 1F



```

1  GACAGCACGC TGCAAGTAGT GGTACGGGTG CGGCCCCCA CCCCTCGGGA GCTGGACAGT
61  CAGCGGCGGC CAGTGGTTCA GGTGGTGGAC GAGCGGGTGC TGGTGTTTAA CCCTGAGGAG
121 CCCGATGGAG GGTTCCTTGG CCTGAAATGG GGTGGCACCC ATGATGGCCC CAAGAAGAAG
181 GGCAAAGACC TGACGTTTGT CTTTGACCGG GTCTTTGGCG AGGCGGCCAC CCAACAGGAC
241 GTGTTCCAGC ACACCACGCA CAGCGTCCTG GACAGCTTCC TCCAGGGCTA CAACTGCTCA
301 GTGTTTGCCT ACGGGGCCAC CGGGGCTGGG AAGACACACA CCATGCTGGG AAGGGAGGGG
361 GACCCCGGCA TCATGTACCT GACCACCGTG GAACTGTACA GGC GCCTGGA GGCCCGCCAG
421 CAGGAGAAGC ACTTCGAGGT GCTCATCAGC TACCAGGAGG TGTATAATGA ACAGATCCAT
481 GACCTCCTGG AGCCCAAGGG GCCCCTTGCC ATCCGCGAGG ACCCCGACAA GGGGGTGGTG
541 GTGCAAGGAC TTTCTTTCCA CCAGCCAGCC TCAGCCGAGC AGCTGCTGGA GATACTGACC
601 AGGGGGAACC GTAACCGCAC GCAGCACCCC ACTGATGCCA ACGCGACTTC CTCCCGCTCC
661 CATGCCATCT TCCAGATCTT TGTGAAGCAG CAGGACCGGG TTCCAGGACT GACCCAGGCT
721 GTCCAGGTGG CCAAGATGAG CCTGATTGAC CTGGCTGGCT CAGAGCGGGC ATCCAGCACC
781 CATGCGAAGG GGGAGCGGCT GCGGGAGGGG GCCAACATCA ACCGCTCTCT GCTGGCGCTC
841 ATCAACGTCC TCAATGCCTT GGCCGATGCA AAGGGCCGCA AGACCCATGT GCCCTACCGG
901 GACAGCAAAC TGACCCGCCT GCTCAAAGAC TCCCTCGGGG GCAACTGCCG CACAGTGATG
961 ATCGCTGCCA TCAGCCCCTC CAGCCTGACC TACGAGGACA CGTACAACAC CCTC

```

FIG. 2

```

1  DSTLQVVVRV RPPTPRELDS QRRPVVQVVD ERVLVFNPEE PDGGFPGLKW GGTHDGPKKK
61  GKDLTFVFDR VFGEAATQQD VFQHTTHSVL DSFLQGYNCS VFAYGATGAG KTHTMLGREG
121 DPGIMYLTTV ELYRRLEARQ QEKHFEVLIS YQEVYNEQIH DLLEPKGPLA IREDPDKGVV
181 VQGLSFHQPA SAEQLLEILT RGNRNRTQHP TDANATSSRS HAIFQIFVKQ QDRVPGLTQA
241 VQVAKMSLID LAGSERASST HAKGERLREG ANINRSLAL INVLNALADA KGRKTHVPYR
301 DSKLTRLLKD SLGGNCRTVM IAAISPSSLT YEDTYNTL

```

FIG. 3



MAVEDSTLQVVVRVRPPTPRELDSQRRPVVQVVDERVLVFNPEEPDGGFPGLKWGGT  
 HDGPKKKGKDLTFVFDRVFGEAATQQDVFQHTTHSVLDSFLQGYNCVVFAYGATGAG  
 KTHTMLGREGDPGIMYLTVELYRRLEARQQEKHFVLI SYQEYVNEQIHDLLEPKG  
 PLAIREDPDKGVVVQGLSFHQPASAEQLLEILTRGNRNRTQHPTDANATSSRSHAI F  
 QIFVKQQDRVPGLTQAVQVAKMSLIDLAGSERASSTHAKGERLREGANINRSLALI  
 NVLNALADAKGRKTHVPYRDSKLTRLKDSLGGNCRTVMIAAISPSSTLYEDTYNTL  
 KYADRAKEIRLKGNSKLEGKPIPNPLLGLDSTRTGHHHHHH

FIG. 4

**AT**GGCAGTGGAGGACAGCACGCTGCAAGTAGTGGTACGGGTGCGGCCCCCACCCT  
 CGGGAGCTGGACAGTCAGCGGCGGCCAGTGGTTCAGGTGGTGGACGAGCGGGTGCTG  
 GTGTTTAACCCTGAGGAGCCCGATGGAGGGTTCCTGGCCTGAAATGGGGTGGCACC  
 CATGATGGCCCCAAGAAGAAGGGCAAAGACCTGACGTTTGTCTTTGACCGGGTCTTT  
 GGCGAGGCGGCCACCCAACAGGACGTGTTCCAGCACACCACGCACAGCGTCCTGGAC  
 AGCTTCCTCCAGGGCTACAACCTGCTCAGTGTTTGCCTACGGGGCCACCGGGGCTGGG  
 AAGACACACACCATGCTGGGAAGGGAGGGGGACCCCGGCATCATGTACCTGACCACC  
 GTGGAACCTGTACAGGCGCCTGGAGGCCCGCCAGCAGGAGAAGCACTTCGAGGTGCTC  
 ATCAGCTACCAGGAGGTGTATAATGAACAGATCCATGACCTCCTGGAGCCCAAGGGG  
 CCCCTTGCCATCCGCGAGGACCCCGACAAGGGGGTGGTGGTGCAAGGACTTTCTTTC  
 CACCAGCCAGCCTCAGCCGAGCAGCTGCTGGAGATACTGACCAGGGGGAACCGTAAC  
 CGCACGCAGCACCCCACTGATGCCAACGCGACTTCCTCCCGCTCCCATGCCATCTTC  
 CAGATCTTTGTGAAGCAGCAGGACCGGGTTCAGGACTGACCCAGGCTGTCCAGGTG  
 GCCAAGATGAGCCTGATTGACCTGGCTGGCTCAGAGCGGGCATCCAGCACCCATGCG  
 AAGGGGGAGCGGCTGCGGGAGGGGGCCAACATCAACCGCTCTCTGCTGGCGCTCATC  
 AACGTCTCAATGCCTTGCCGATGCAAAGGGCCGCAAGACCCATGTGCCCTACCGG  
 GACAGCAAACCTGACCCGCCTGCTCAAAGACTCCCTCGGGGGCAACTGCCGCACAGTG  
 ATGATCGCTGCCATCAGCCCCCTCCAGCCTGACCTACGAGGACACGTACAACACCCTC  
 AAATATGCCGACCGGGCCAAGGAGATCAGGCTCAAGGGCAATTGGAAGCTGAAGGT  
 AAGCCTATCCCTAACCCTCTCCTCGGTCTCGATTCTACGCGTACCGGTCATCATCAC  
 CATCACCATTGA

FIG. 5



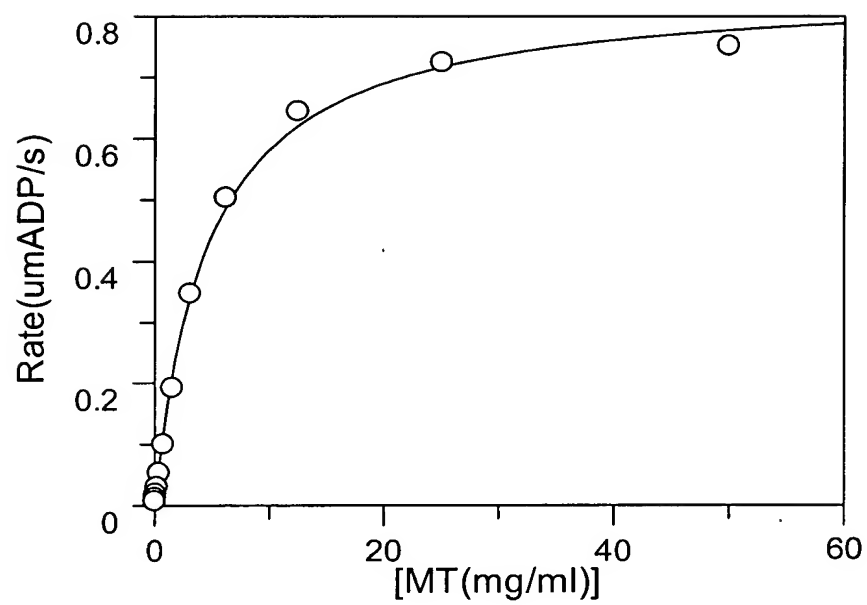


FIG. 6

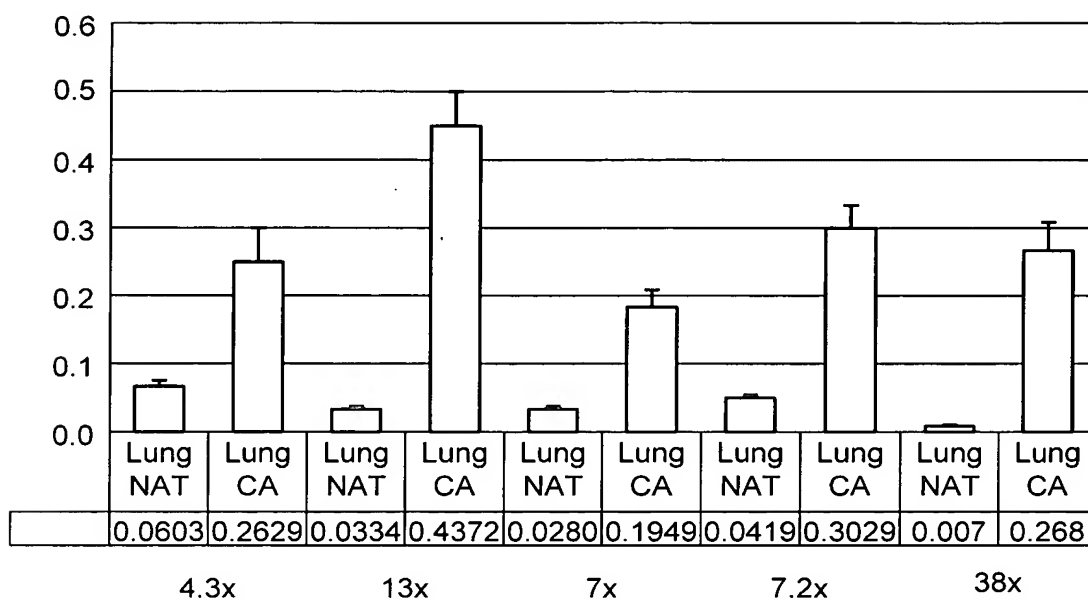


FIG. 7A

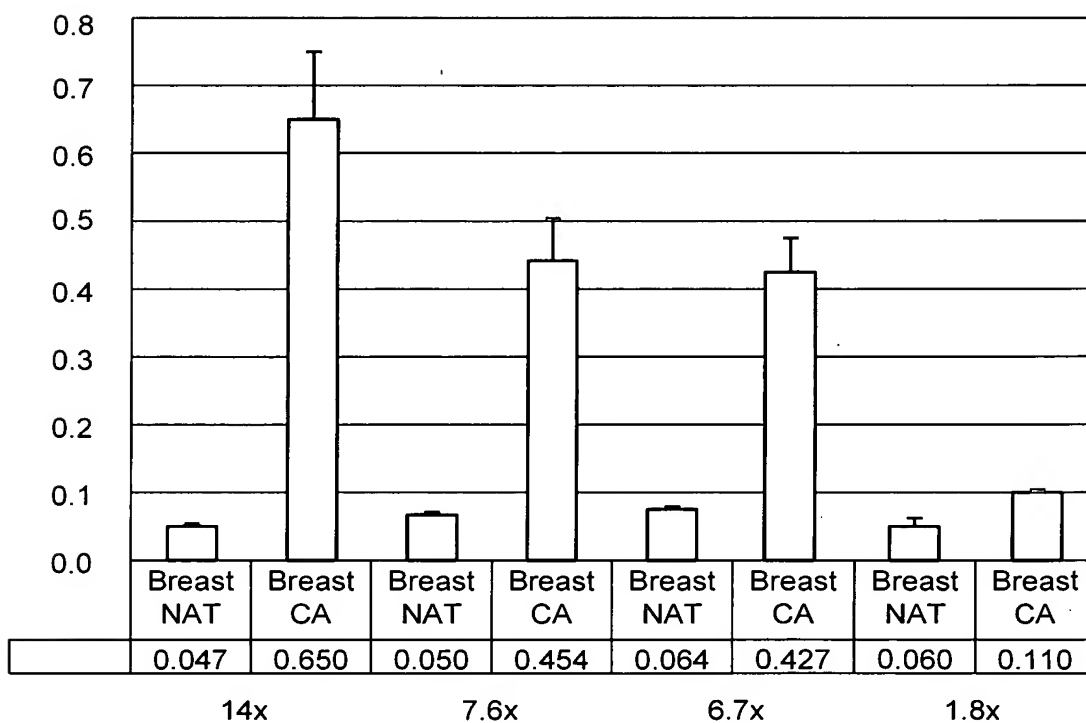


FIG. 7B

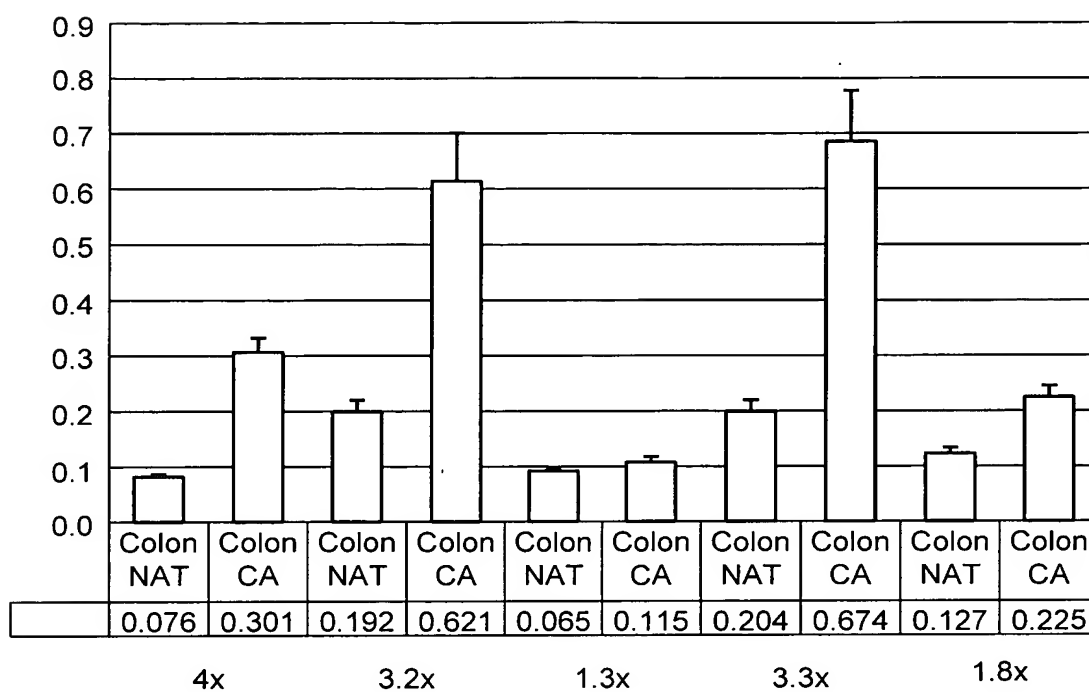


FIG. 7C

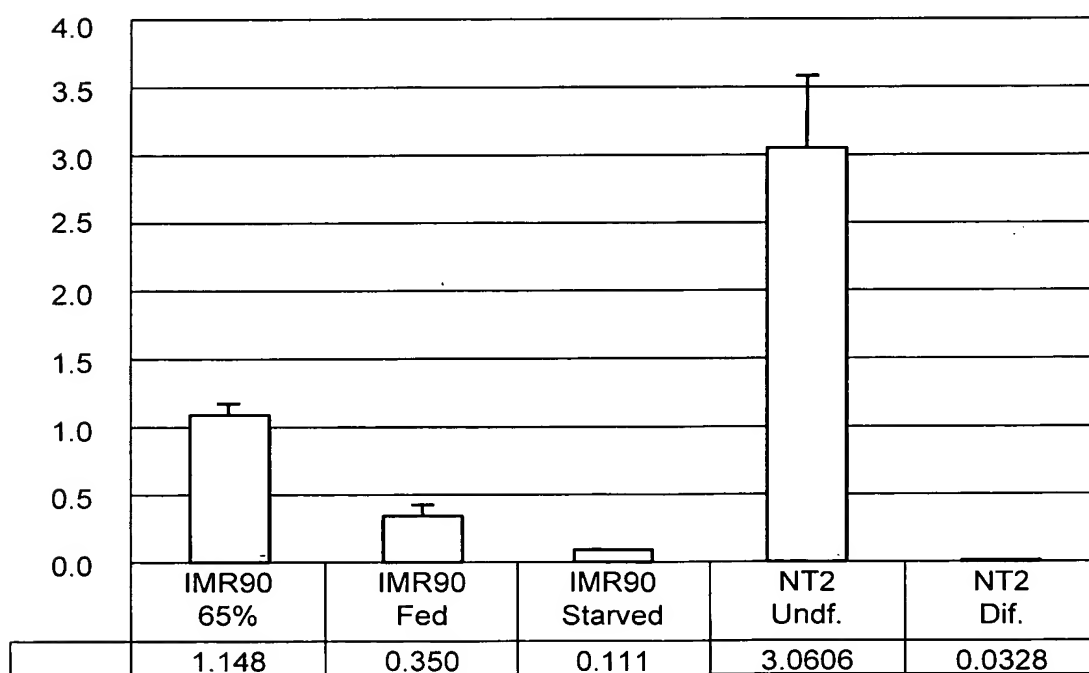


FIG. 7D